AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1 – 27 (Cancelled)

28. (Currently amended) A medicinal product, which comprises an active component selected from the group consisting of:

a) a protein, ASAP, selected from the group consisting of a human protein of sequence SEQ ID NO: 1 and ~~the~~ proteins for which ~~the~~ a sequence thereof exhibits at least 80% identity or at least 90% similarity, with the entire sequence SEQ ID NO: 1,

b) a peptide of at least 10 consecutive amino acids of the protein defined in a),

c) a monoclonal or polyclonal antibody capable of specifically recognizing the

protein defined in a) or the peptide defined in b),

d) a polynucleotide encoding the protein defined in a) or the peptide defined in b), or a polynucleotide that is antisense to the preceding polynucleotide,

e) a polynucleotide fragment of at least 15 consecutive nucleotides of the polynucleotide defined in d) or a fragment that is antisense to the preceding fragment,

f) an expression vector comprising the polynucleotide defined in d) or the fragment defined in e), and

g) a host cell transformed with the polynucleotide defined in d), the fragment

defined in e) or the vector defined in f).

29. (Previously presented) The medicinal product of Claim 28, wherein said the sequence of a) exhibits at least 90% identity or at least 95% similarity with the entire sequence SEQ ID No.: 1.

30. (Previously presented) The medicinal product of Claim 28, wherein said polynucleotide or said fragment is selected from the group consisting of sequences SEQ ID NOs: 15 to 30 and 45, and sequences which are antisense to the preceding sequences.

31. (Previously presented) The medicinal product of Claim 28, wherein said protein or said peptide is selected from the group consisting of sequences SEQ ID NOS: 2 to 14 and 46 to 53.

32. (Previously presented) The medicinal product of Claim 28, wherein said antibody specifically recognizes protein of sequence SEQ ID NO: 1 or 46, or at least one of the peptides of sequence SEQ ID NOS: 2 to 14 and 47 to 53.

33. (Previously presented) A method of preparing an anti-mitotic medicinal product, which comprises selecting at least one active component of Claim 28, and preparing the anti-mitotic medicinal product therewith.

34. (Previously presented) A method of preparing a medicinal product for treating pathologies associated with disturbances in mitotic spindle organization or with induction of aberrant and abortive mitoses associated with overexpression of ASAP protein, which comprises selecting at least one active component as defined of claim 28, and preparing the medicinal product therewith.

35. (Previously presented) A method of diagnosing pathological states or genetic diseases associated with disturbances in mitotic spindle organization or cell

division anomalies or both, which comprises probing for said states or diseases or both with the polynucleotide or polynucleotide fragment of Claim 28.

36. (Previously presented) The method of Claim 35, wherein the probe is selected from the group consisting of: sequences SEQ ID NOS: 15, 17 to 44, sequences listed under the accession numbers AK024730 and AK024812, and ESTs listed under the accession numbers BU198882, BM693711,

AW372449, BM021380, BU928828, AL707573, AI885274, AI671785, AA805679, BU619959. BM021126, AL598336, AW976973, BU629726, AI433877, AV751613. BQ372751, AI827535, AI866257, AA843565, R96130.

BU684090, BF958121, BQ351941, AW194906, BG203580, BF078132, AW486134, AL600279, AA025538, AL600264, BF170676, BU759494, BB025236, BF214179, AI283076, BE694273, AI266380, BM670854, AA968415, BU503982, BB700612, BE988355, BU058357, BB312934, AW061311, BM537962, BE988356, BB318982, BB311217, BB557152, BB185248, BB557128, BB698742, BB186736, AV345769, BB274293, BB632007, BB617958. AI391312, W18534, BB186581, BB311289, BB312835, AW347411, AA972439, BB263570, AU035125, BB277226, BB274224, BB268445, AW024037, AA025609, BB274174, R96089, BB272238, BB269037, BB385718, BE007324, BB325992, AJ275277, AI414381, BB125476, BB430961, BE232162, BQ121419, BQ121418, BG591509, BF457670, AL897593. AL897592, BM926692. BM538559, BI759567, AL601021, AL598780. AU222540, BG567619, AU166296,

BF889835, AU164011, AV656025, BF343454, AW262441, AW237952 in the GenBank database, and the fragments of at least 15 consecutive nucleotides of the preceding sequences.

37. (Previously presented) A method of detecting or selecting cells or both exhibiting disturbances in mitotic spindle organization or induction of aberrant and

abortive mitoses associated with overexpression of the protein of Claim 28, which comprises detecting or selecting cells using an antibody as defined in Claim 28.

38. (Previously presented) An isolated protein, ASAP, which is a human protein of sequence SEQ ID NO: 1 or a murine protein of sequence SEQ ID NO: 46.

39. (Previously presented) A peptide, which consists of a fragment of the protein of Claim 38, selected from the group consisting of sequences SEQ ID NO: 2 to SEQ ID NO: 14 and 47 to 53.

40. (Previously presented) A monoclonal or polyclonal antibody, which recognizes, among microtubule-associated proteins or MAPs, only and specifically the protein of Claim 38, or one or more peptides of Claim 39.

41. (Previously presented) An isolated polynucleotide, which is selected from the group consisting of:

a) the cDNA of sequence SEQ ID NO: 15 encoding the human ASAP protein of Claim 38,

b) the cDNA of sequence SEQ ID NO: 45 encoding the murine ASAP protein of Claim 38,

c) a genomic DNA fragment of 29800 nucleotides having the sequence SEQ ID NO: 16, corresponding to the human *asap* gene, and

d) polynucleotides complementary to the preceding polynucleotides, which are either sense or antisense.

42. (Previously presented) A fragment of the polynucleotide of Claim 41, is selected from the group consisting of probes of sequence SEQ ID NOS: 17 to 30.

43. (Previously presented) A primer for amplifying the polynucleotide of Claim 28, which is selected from the group consisting of the sequences SEQ ID NOS: 31 to 43.

44. (Previously presented) A cloning or expression vector or both, which comprises an insert consisting of a polynucleotide of Claim 41, or a fragment of Claim 42.

45. (Previously presented) A host cell, which is transformed with a polynucleotide of Claim 41, a fragment of Claim 42, or a vector of Claim 43.

46. (Previously presented) A nonhuman transgenic organism, wherein all or some of cells thereof comprise at least one polynucleotide of Claim 41, one fragment or one vector of Claim 44, in free or integrated form.

47. (Previously presented) The nonhuman transgenic organism of Claim 46, wherein said cells comprise a polynucleotide of Claim 41, or a fragment of Claim 42, that is nonfunctional or contains a mutation.

48. (Previously presented) A method for diagnosing a pathological state associated with disturbances in mitotic spindle organization or with cell division anomalies or both, which comprises determining an alteration of a transcription profile of the gene encoding the ASAP protein comprising at least the steps of:

a) a first step of obtaining a total RNA from a biological sample,

b) a second step of bringing said RNA into contact with a probe of Claim 35, 36 or 42, labeled beforehand, under conditions for hybridization between the RNAs and the probe, and

c) a third step of detecting the hybrids formed.

49. (Previously presented) The method of Claim 48, wherein step b) is a step consisting of reverse transcription or amplification of the transcripts or both, carried out using a pair of primers of Claim 43, and the third step is a step consisting in detecting the amplified nucleic acids.

50. (Previously presented) The method of Claim 48 which further comprises a step consisting of evaluating the level of transcription of the gene by comparison with a control selected beforehand.

51. (Previously presented) A method for diagnosing a genetic disease associated with disturbances in mitotic spindle organization or with cell division anomalies or both, which comprises demonstrating a functional alteration of the gene encoding the ASAP protein of Claim 28, according to at least the following steps:

a) a first step of obtaining DNA from a biological sample,

b) a second step of bringing said DNAs into contact with a probe labeled beforehand, under conditions for hybridization between the DNAs and the probe, and

c) a third step of detecting the hybrids formed.

52. (Previously presented) The method of Claim 51, wherein the second step is an amplification step carried out using a pair of primers of Claim 43, and the third step is a step of detecting the amplified nucleic acids formed.

53. (Previously presented) The method of Claim 50, further comprising a step of isolating and sequencing the nucleic acids demonstrated.

54. (Previously presented) The method of Claim 51, further comprising a step of isolating and sequencing the nucleic acids demonstrated.

55. (Previously presented) A method for evaluating, *in vitro*, a proliferative capacity or aggressiveness of cancer cells, comprising:

a) a first step comprising treating cells for making the intracellular medium accessible,

b) a second step comprising bringing said intracellular medium thus obtained into contact with an antibody of Claims 28, 32 or 40.

c) a third step comprising the ASAP protein-antibody complex formed, and

d) a fourth step comprising evaluating the level of transcription of the gene by comparison of the level of ASAP protein-antibody complexes formed with that of a control biological sample selected beforehand.

56. (Currently amended) A method of screening for a substance capable of modulating ~~the~~ activity of ~~the protein:~~ a protein, ASAP, selected from the group consisting of a human protein of sequence SEQ ID No: 1 and proteins for which a sequence thereof exhibits at least 80% identity or at least 90% similarity with an entire sequence of SEQ ID No: 1, which method comprises:

a) contacting, in a first step, cells of a biological sample expressing ~~the protein of Claim 28, are brought into contact~~ said ASAP protein with a substance to be tested,

b) measuring, in a second step, the effect of said substance on mitotic spindle organization or ~~the~~ induction of aberrant and abortive mitoses ~~is measured~~, and

c) selecting, in a third step, substances capable of modulating said activity ~~are selected~~.

57. (Currently amended) The method of Claim ~~55~~ 56, wherein said modulating is activating.

58. (Previously presented) The method of Claim 56, wherein said modulating is inhibiting.

59. (New) The method of Claim 56, wherein the ASAP protein which is expressed is the murine ASAP (SEQ ID No: 46).

60. (New) The method of Claim 56, wherein the cells of the biological sample expressing the ASAP protein are transformed host cells over-expressing a recombinant ASAP protein.

61. (New) The method of Claim 60, wherein the recombinant ASAP protein is an ASAP protein fused with a fluorescent protein.